WHAT IS CLAIMED IS:

1. A method of identifying sequences in a polynucleotide sequence, comprising:

first cleaving the polynucleotide sequence with a first type-IIs endonuclease;

first ligating a first adapter sequence to the polynucleotide sequence cleaved in said first cleaving step, said first adapter having a recognition site for a second type-IIs endonuclease;

second cleaving the polynucleotide sequence resulting from said first ligating step, with the second type-IIs endonuclease;

second ligating a second adapter sequence to the polynucleotide sequence cleaved in said second cleaving step; and

determining the sequence of nucleotides of the polynucleotide sequence between the first and second adapter sequences.

2. The method of claim 1, wherein:

in said first cleaving step, the first type-IIs endonuclease is selected from the group consisting of BsmAI, EarI, MnlI, PleI, AlwI, BbsI, BsaI, BspMI, Esp3I, HgaI, SapI, SfaNI, BseRI, HphI and MboII; and

in said second cleaving step, the second type-IIs endonuclease is selected from the group consisting of HgaI, BbvI, BspMI, BsmFI and FokI.

3. The method of claim 2, wherein

in said first cleaving step, the first type-IIs endonuclease is EarI; and

in said second cleaving step, the second type-IIs endonuclease is HgaI.

4. The method of claim 1, wherein in said first and second ligating steps, said first and second adapter sequences comprise primer sequences.

5. The method of claim 4, wherein prior to said determining step, the sequence of oligonucleotides in the polynucleotide between the first and second adapter sequences is amplified.

6. The method of claim 1, wherein in said determining step, the sequence of nucleotides between the first and second adapter sequences is determined by hybridization to an oligonucleotide probe.

7. The method of claim 6, wherein said oligonucleotide probe is a positionally distinct probe on an oligonucleotide array, a position of the probe being indicative of the sequence of the probe.

8. A method of generating an ordered map of a library of genomic fragments, the method comprising:

identifying sequences in each of the genomic fragments in the library, according to the method of claim 1;

comparing the sequences identified in each fragment with the sequences identified in each other fragment to obtain a level of correlation between each fragment and each other fragment; and

ordering the fragments according to their level of correlation.

9. A method of identifying polymorphisms in a target polynucleotide sequence, the method comprising:

identifying sequences in a wild-type polynucleotide sequence, according to the method of claim 1,

repeating said identifying step on the target polynucleotide sequence; and

determining differences in the sequences identified in each of said identifying steps, the differences being indicative of a polymorphism.

10. The method of claim 1, wherein said sequences in a polynucleotide sequence are proximal to a polymorphism.

11. A method of identifying a source of a biological sample, the method comprising:

identifying a plurality of sequences in a polynucleotide sequence derived from the sample, according to the method of claim 1; and

comparing the plurality of sequences identified in said identifying step with a plurality of sequences identically identified from a polynucleotide derived from a known source, identity of the plurality of sequences identified from the sample with the plurality of sequences identified from the known source being indicative that the sample was derived from the known source.

12. A method of determining a relative location of a target nucleotide sequence on a polynucleotide, the method comprising:

generating an ordered map of the polynucleotide according to the method of claim 8;

fragmenting the polynucleotide;

determining which fragment includes the target nucleotide sequence;

correlating a marker on the fragment with a marker on the ordered map to identify the approximate location of the target nucleotide sequence on the polynucleotide.